

RAW SEQUENCE LISTING
ERROR REPORT

BIO. TECHNOLOGY
SYSTEMS
BRANCH

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1633
117

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/602 362 B

Source: AU 1600

Date Processed by STIC: 11/14/01

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE US PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

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Checker Version 3.0

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The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/602,362B

DATE: 11/14/2001

TIME: 13:47:29

Input Set : A:\#661413 v2 - LUD 5615.1 SEQ LISTING.txt
Output Set: N:\CRF3\11142001\I602362B.raw

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1 <110> APPLICANT: Jager, Dirk
 2 Scanlan, Matthew
 3 Gure, Ali
 4 Jager, Elke
 5 Knuth, Alexander
 6 Old, Lloyd
 7 Chen, Yao-tseng
 9 <120> TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
 Antigens,
 10 the Antigens per se, and Uses Thereof
 12 <130> FILE REFERENCE: LUD 5615.1
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/602,362B
 C--> 16 <141> CURRENT FILING DATE: 2001-11-13
 18 <150> PRIOR APPLICATION NUMBER: 09/451,739
 20 <151> PRIOR FILING DATE: 1999-11-30
 22 <160> NUMBER OF SEQ ID NOS: 29

Does Not Comply
Corrected Diskette Needed

See page 2 and page 2 of 5B

ERRORED SEQUENCES

519 <210> SEQ ID NO: 16
 520 <211> LENGTH: 513
 521 <212> TYPE: PRT
 522 <213> ORGANISM: Homo sapiens
 W--> 523 <400> SEQUENCE: 16

524	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala	Leu	Glu	Leu	Met	Asp	Met	Gln
525	1			5						10					15	
527	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys	Pro	Ser	Ala	Phe	Glu	Pro	Ala
528				20				25						30		
530	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn	Lys	Ala	Leu	Glu	Leu	Lys	Asn
531				35				40					45			
533	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Glu	Ile	Leu	Pro	Ser	Glu	Ser	Lys	Gln
534				50				55					60			
536	Lys	Asp	Tyr	Glu	Glu	Ser	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr
537	65					70				75					80	
539	Val	Ser	Gln	Lys	Asp	Val	Cys	Leu	Pro	Lys	Ala	Thr	His	Gln	Lys	Glu
540				85					90					95		
542	Ile	Asp	Lys	Ile	Asn	Gly	Lys	Leu	Glu	Glu	Ser	Pro	Asp	Asn	Asp	Gly
543				100					105					110		
545	Phe	Leu	Lys	Ala	Pro	Cys	Arg	Met	Lys	Val	Ser	Ile	Pro	Thr	Lys	Ala
546				115				120						125		
548	Leu	Glu	Leu	Met	Asp	Met	Gln	Thr	Phe	Lys	Ala	Glu	Pro	Pro	Glu	Lys
549				130				135					140			
551	Pro	Ser	Ala	Phe	Glu	Pro	Ala	Ile	Glu	Met	Gln	Lys	Ser	Val	Pro	Asn
552	145					150				155					160	
554	Lys	Ala	Leu	Glu	Leu	Lys	Asn	Glu	Gln	Thr	Leu	Arg	Ala	Asp	Gln	Met
555				165					170						175	
557	Phe	Pro	Ser	Glu	Ser	Lys	Gln	Lys	Lys	Val	Glu	Glu	Asn	Ser	Trp	Asp

Errored Input 513 and Found 512
 Include sample from diskette of 220-223 errors

RAW SEQUENCE LISTING

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558 180 185 190
560 Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro
561 195 200 205
563 Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu
564 210 215 220
566 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
567 225 230 235 240
569 Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys
570 245 250 255
572 Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser
573 260 265 270
575 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp
576 275 280 285
578 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu
579 290 295 300
581 Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu
582 305 310 315 320
584 Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln
585 325 330 335
587 Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu
588 340 345 350
590 Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu
E--> 591 325 360 365
593 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
594 370 375 380
596 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr
597 385 390 395 400
599 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met
600 405 410 415
602 Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr
603 420 425 430
605 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser
606 435 440 445
609 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu
610 450 455 460
612 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile
613 465 470 475 480
615 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp
616 485 490 495
618 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile
E--> 619 500 505 510

355

Input 513 in field 211
Found only 512 and 619

9/602 362B 245B

<210> 15
<211> 2030
<212> DNA
<213> Homo sapiens
<221> CDS
<222> 1628, 1752, 1758, 1769, 1789, 1873, 1908, 1915, 1933, 1970, 1976, 2022
<400> 15

Field 220 - a header field
Field 220 must precede
Fields 221 and 222

ctcgtgccgt taaagatggt cttctgaagg ctaactgcgg aatgaaagtt tctattccaa 60
ctaaagcctt agaattgatg gacatgcaaa ctttcaaagc agagcctccc gagaagccat 120
ctgccttcga gcctgccatt gaaatgcaaa agtctgttcc aaataaagcc ttggaattga 180
agaatgaaca aacattgaga gcagatgaga tactcccatc agaatccaaa caaaaggact 240
atgaagaaag ttctgggat tctgagagtc tctgtgagac tgtttcacag aaggatgtgt 300
gtttacccaa ggctacacat caaaaagaaa tagataaat aaatggaaaa ttagaagagt 360

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- ① looks like contents as of
19 Nov 01
- ② Sequence ID NO 15
Header Field 220 is
mandatory
- ③ Field 223 desired,
but not required
- ④ * No artificial sequences
in listing.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/602,362B

DATE: 11/14/2001

TIME: 13:47:31

Input Set : A:\#661413 v2 - LUD 5615.1 SEQ LISTING.txt

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L:14 M:270 C: Current Application Number differs, Replaced Application Number
 L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:29 M:283 W: Missing Blank Line separator, <220> field identifier
 L:32 M:283 W: Missing Blank Line separator, <400> field identifier
 L:39 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
 L:39 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
 L:90 M:283 W: Missing Blank Line separator, <400> field identifier
 L:169 M:283 W: Missing Blank Line separator, <400> field identifier
 L:205 M:283 W: Missing Blank Line separator, <400> field identifier
 L:265 M:283 W: Missing Blank Line separator, <400> field identifier
 L:313 M:283 W: Missing Blank Line separator, <400> field identifier
 L:366 M:283 W: Missing Blank Line separator, <400> field identifier
 L:389 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
 L:389 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
 L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
 L:398 M:283 W: Missing Blank Line separator, <400> field identifier
 L:415 M:283 W: Missing Blank Line separator, <400> field identifier
 L:423 M:283 W: Missing Blank Line separator, <400> field identifier
 L:431 M:283 W: Missing Blank Line separator, <400> field identifier
 L:439 M:283 W: Missing Blank Line separator, <400> field identifier
 L:449 M:283 W: Missing Blank Line separator, <400> field identifier
 L:504 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
 L:504 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
 L:504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:508 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
 L:508 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
 L:508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:512 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
 L:512 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
 L:512 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:514 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
 L:514 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
 L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:516 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
 L:516 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
 L:516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
 L:523 M:283 W: Missing Blank Line separator, <400> field identifier
 L:591 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
 L:619 M:252 E: No. of Seq. differs, <211>LENGTH:Input:513 Found:512 SEQ:16
 L:626 M:283 W: Missing Blank Line separator, <400> field identifier
 L:634 M:283 W: Missing Blank Line separator, <400> field identifier
 L:642 M:283 W: Missing Blank Line separator, <400> field identifier
 L:705 M:283 W: Missing Blank Line separator, <400> field identifier
 L:712 M:283 W: Missing Blank Line separator, <400> field identifier
 L:720 M:283 W: Missing Blank Line separator, <400> field identifier
 L:863 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1121 M:283 W: Missing Blank Line separator, <400> field identifier
 L:1128 M:283 W: Missing Blank Line separator, <400> field identifier

Example sequence 16

not needed

VERIFICATION SUMMARY

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L:1138 M:283 W: Missing Blank Line separator, <400> field identifier
L:1153 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:1153 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1153 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1197 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:26
L:1197 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:26
L:1197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1268 M:283 W: Missing Blank Line separator, <400> field identifier
L:1466 M:283 W: Missing Blank Line separator, <400> field identifier
L:1474 M:283 W: Missing Blank Line separator, <400> field identifier

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} Errored